

PCT10

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/009,782

DATE: 01/14/2002

TIME: 07:53:45

Input Set : A:\217301US0PCT.txt

Output Set: N:\CRF3\01142002\J009782.raw

ENTERED

3 <110> APPLICANT: TAKEUCHI, Ken-ichi
4 KOIDE, Yoshinao
5 HIROSE, Yoshihiko
6 MORIGUCHI, Mitsuaki
7 ISOBE, Kimiyasu
9 <120> TITLE OF INVENTION: TRANSFORMED MICROORGANISM AND PROCESS FOR PRODUCING D-AMINOACYLASE
11 <130> FILE REFERENCE: 217301US0PCT
C--> 13 <140> CURRENT APPLICATION NUMBER: US/10/009,782
C--> 13 <141> CURRENT FILING DATE: 2001-12-17
13 <150> PRIOR APPLICATION NUMBER: PCT/JP00/03932
14 <151> PRIOR FILING DATE: 2000-06-15
16 <160> NUMBER OF SEQ ID NOS: 2
18 <170> SOFTWARE: PatentIn version 3.1
20 <210> SEQ ID NO: 1
21 <211> LENGTH: 1758
22 <212> TYPE: DNA
23 <213> ORGANISM: Alcaligenes xylosoxydans subsp. xylosoxydans
25 <220> FEATURE:
26 <221> NAME/KEY: CDS
27 <222> LOCATION: (34)..(1485)
28 <223> OTHER INFORMATION:
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33 Met Ser Gln Ser Asp Ser Gln
34 1 5
36 ccc ttc gac ctg ctg ctc gcg ggc ggc acc ctc atc gac ggc agc aac. 102
37 Pro Phe Asp Leu Leu Leu Ala Gly Gly Thr Leu Ile Asp Gly Ser Asn
38 10 15 20
40 acc ccg ggg cgg cgc gcc gac ctg ggc gtg cgc ggc gac cgc atc gcc 150
41 Thr Pro Gly Arg Arg Ala Asp Leu Gly Val Arg Gly Asp Arg Ile Ala
42 25 30 35
44 gcc atc ggc gat ctg tgc gac gcc gcc gcg cac acc cgg gtc gac gtg 198
45 Ala Ile Gly Asp Leu Ser Asp Ala Ala Ala His Thr Arg Val Asp Val
46 40 45 50 55
48 tgc ggc ctg gtg gtc gcg ccc ggc ttc atc gac tgc cac acc cac gac 246
49 Ser Gly Leu Val Val Ala Pro Gly Phe Ile Asp Ser His Thr His Asp
50 60 65 70
52 gac aac tac ctg ctc agg cgt cgc gac atg acg ccc aag atc tgc cag 294
53 Asp Asn Tyr Leu Leu Arg Arg Arg Asp Met Thr Pro Lys Ile Ser Gln
54 75 80 85
56 ggc gtc acc acg gtg gtc acg ggc aat tgc ggc atc agc ctg gcg ccg 342
57 Gly Val Thr Thr Val Val Thr Gly Asn Cys Gly Ile Ser Leu Ala Pro
58 90 95 100
60 ctg gcg cac gcc aac ccg ccc gcc ccc ctg gac ctg ctg gac gaa ggc 390
61 Leu Ala His Ala Asn Pro Pro Ala Pro Leu Asp Leu Leu Asp Glu Gly
62 105 110 115
64 ggc tct tac cgt ttc gag cgc ttc gcc gac tac ctg gac gcg ttg cgg 438

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65	Gly	Ser	Tyr	Arg	Phe	Glu	Arg	Phe	Ala	Asp	Tyr	Leu	Asp	Ala	Leu	Arg	
66	120					125					130					135	
68	gcc	acg	ccg	gcg	gcc	gtc	aac	gcc	gcc	tgt	atg	gtg	ggc	cat	tca	acg	486
69	Ala	Thr	Pro	Ala	Ala	Val	Asn	Ala	Ala	Cys	Met	Val	Gly	His	Ser	Thr	
70					140					145						150	
72	ctg	cgc	gcc	gcg	gtc	atg	ccg	gac	ttg	cag	cgc	gcc	gcc	acc	gac	gag	534
73	Leu	Arg	Ala	Ala	Val	Met	Pro	Asp	Leu	Gln	Arg	Ala	Ala	Thr	Asp	Glu	
74					155				160					165			
76	gaa	atc	gcg	gcc	atg	cgg	gac	ctg	gcc	gag	gaa	gcc	atg	gcc	agc	ggc	582
77	Glu	Ile	Ala	Ala	Met	Arg	Asp	Leu	Ala	Glu	Glu	Ala	Met	Ala	Ser	Gly	
78			170					175						180			
80	gcc	atc	ggc	att	tcg	acc	ggc	gcc	ttc	tac	ccg	ccc	gcc	gcc	cgc	gcc	630
81	Ala	Ile	Gly	Ile	Ser	Thr	Gly	Ala	Phe	Tyr	Pro	Pro	Ala	Ala	Arg	Ala	
82		185					190					195					
84	acc	acc	gaa	gag	atc	atc	gag	gtg	tgc	cgg	ccg	ctg	agc	gcg	cat	ggc	678
85	Thr	Thr	Glu	Glu	Ile	Ile	Glu	Val	Cys	Arg	Pro	Leu	Ser	Ala	His	Gly	
86	200					205					210				215		
88	ggc	atc	tac	gcc	acc	cac	atg	cgc	gac	gaa	ggc	gag	cac	atc	gtg	gcc	726
89	Gly	Ile	Tyr	Ala	Thr	His	Met	Arg	Asp	Glu	Gly	Glu	His	Ile	Val	Ala	
90				220					225					230			
92	gcg	ctg	gag	gaa	acc	ttc	cgc	atc	ggc	cgc	gag	ctg	gac	gtg	ccg	gtg	774
93	Ala	Leu	Glu	Glu	Thr	Phe	Arg	Ile	Gly	Arg	Glu	Leu	Asp	Val	Pro	Val	
94			235					240					245				
96	gtg	atc	tcg	cac	cac	aag	gtc	atg	ggc	cag	ccc	aat	ttc	ggc	cgc	tcg	822
97	Val	Ile	Ser	His	His	Lys	Val	Met	Gly	Gln	Pro	Asn	Phe	Gly	Arg	Ser	
98		250					255			260							
100	cgc	gag	acg	ctg	ccg	ctg	atc	gag	gcc	gcc	atg	gcg	cgc	cag	gac	gtc	870
101	Arg	Glu	Thr	Leu	Pro	Leu	Ile	Glu	Ala	Ala	Met	Ala	Arg	Gln	Asp	Val	
102		265					270				275						
104	tcg	ctg	gac	gcg	tat	ccc	tac	gtg	gcc	ggc	tcc	acc	atg	ctc	aag	cag	918
105	Ser	Leu	Asp	Ala	Tyr	Pro	Tyr	Val	Ala	Gly	Ser	Thr	Met	Leu	Lys	Gln	
106	280					285					290				295		
108	gac	cgc	gtg	ctg	ctg	gcc	gga	cgc	acc	atc	atc	acc	tgg	tgc	aag	ccc	966
109	Asp	Arg	Val	Leu	Leu	Ala	Gly	Arg	Thr	Ile	Ile	Thr	Trp	Cys	Lys	Pro	
110				300					305					310			
112	ttc	ccc	gaa	ctg	agc	ggg	cgc	gac	ctg	gat	gaa	gtc	gcg	gcc	gag	cgc	1014
113	Phe	Pro	Glu	Leu	Ser	Gly	Arg	Asp	Leu	Asp	Glu	Val	Ala	Ala	Glu	Arg	
114			315					320					325				
116	ggc	aaa	tcc	aag	tac	gac	gtg	gtg	ccc	gag	ctg	cag	ccg	gcc	ggc	gcc	1062
117	Gly	Lys	Ser	Lys	Tyr	Asp	Val	Val	Pro	Glu	Leu	Gln	Pro	Ala	Gly	Ala	
118		330					335					340					
120	atc	tac	ttc	atg	atg	gac	gaa	ccc	gac	gtg	cag	cgc	atc	ctg	gcg	ttc	1110
121	Ile	Tyr	Phe	Met	Met	Asp	Glu	Pro	Asp	Val	Gln	Arg	Ile	Leu	Ala	Phe	
122		345				350					355						
124	ggc	ccg	acc	atg	atc	ggc	tcc	gac	ggc	ctg	ccg	cac	gac	gag	cgc	ccg	1158
125	Gly	Pro	Thr	Met	Ile	Gly	Ser	Asp	Gly	Leu	Pro	His	Asp	Glu	Arg	Pro	
126	360					365				370					375		
128	cat	ccg	cgc	ctg	tgg	ggc	acc	ttc	ccg	cgg	gtg	ctg	ggg	cac	tat	gcg	1206
129	His	Pro	Arg	Leu	Trp	Gly	Thr	Phe	Pro	Arg	Val	Leu	Gly	His	Tyr	Ala	

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130                               380                               385                               390
132 cgc gac ctg ggc ctg ttc ccg ctg gag acg gcg gta tgg aag atg acc      1254
133 Arg Asp Leu Gly Leu Phe Pro Leu Glu Thr Ala Val Trp Lys Met Thr
134                               395                               400                               405
136 ggc ctg acc gcc gcg cgc ttc ggc ctg gcc ggg cgc ggg cag ctg cag      1302
137 Gly Leu Thr Ala Ala Arg Phe Gly Leu Ala Gly Arg Gly Gln Leu Gln
138                               410                               415                               420
140 gcc ggg tac ttc gcc gac ctg gtg gtg ttc gac ccg gcc acg gtg gcc      1350
141 Ala Gly Tyr Phe Ala Asp Leu Val Val Phe Asp Pro Ala Thr Val Ala
142                               425                               430                               435
144 gat acc gcc acc ttc gaa cac cct acc gag cgc gcc gcc ggc atc cat      1398
145 Asp Thr Ala Thr Phe Glu His Pro Thr Glu Arg Ala Ala Gly Ile His
146 440~                               445                               450                               455
148 tcc gtg tac gtc aac ggc gcg ccg gtc tgg caa gag cag gcg ttc acc      1446
149 Ser Val Tyr Val Asn Gly Ala Pro Val Trp Gln Glu Gln Ala Phe Thr
150                               460                               465                               470
152 ggc cag cat gcc ggc cgc gtg ctc gca cgc acg gcc gcc tgagcccggc      1495
153 Gly Gln His Ala Gly Arg Val Leu Ala Arg Thr Ala Ala
154                               475                               480
156 gccagccctt acaatccggc gtgaacgggg cggcgtgccg cccctccca accctggacg      1555
158 caaaccgcta catggcccct cctccgctc gcaatacggc cccaccgat atcgtgggca      1615
160 aggaagtgat gggcgcgcg ctcgcgccg agcgcaaggc cgggaaaatg accctgcaag      1675
162 acctgtcgca ggccagcggc atcgcggtct cgaccctgtc caaggccgag ctgggcccaga      1735
164 tcgccctgag ctacgagaag ctt
167 <210> SEQ ID NO: 2
168 <211> LENGTH: 484
169 <212> TYPE: PRT
170 <213> ORGANISM: Alcaligenes xylosoxydans subsp. xylosoxydans
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178 Thr Leu Ile Asp Gly Ser Asn Thr Pro Gly Arg Arg Ala Asp Leu Gly
179                               20                               25                               30
182 Val Arg Gly Asp Arg Ile Ala Ala Ile Gly Asp Leu Ser Asp Ala Ala
183                               35                               40                               45
186 Ala His Thr Arg Val Asp Val Ser Gly Leu Val Val Ala Pro Gly Phe
187                               50                               55                               60
190 Ile Asp Ser His Thr His Asp Asp Asn Tyr Leu Leu Arg Arg Arg Asp
191 65                               70                               75                               80
194 Met Thr Pro Lys Ile Ser Gln Gly Val Thr Thr Val Val Thr Gly Asn
195                               85                               90                               95
198 Cys Gly Ile Ser Leu Ala Pro Leu Ala His Ala Asn Pro Pro Ala Pro
199                               100                              105                              110
202 Leu Asp Leu Leu Asp Glu Gly Gly Ser Tyr Arg Phe Glu Arg Phe Ala
203                               115                              120                              125
206 Asp Tyr Leu Asp Ala Leu Arg Ala Thr Pro Ala Ala Val Asn Ala Ala
207                               130                              135                              140
210 Cys Met Val Gly His Ser Thr Leu Arg Ala Ala Val Met Pro Asp Leu
211 145                              150                              155                              160

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214 Gln Arg Ala Ala Thr Asp Glu Glu Ile Ala Ala Met Arg Asp Leu Ala
215                               165                               170                               175
218 Glu Glu Ala Met Ala Ser Gly Ala Ile Gly Ile Ser Thr Gly Ala Phe
219                               180                               185                               190
222 Tyr Pro Pro Ala Ala Arg Ala Thr Thr Glu Glu Ile Ile Glu Val Cys
223                               195                               200                               205
226 Arg Pro Leu Ser Ala His Gly Gly Ile Tyr Ala Thr His Met Arg Asp
227                               210                               215                               220
230 Glu Gly Glu His Ile Val Ala Ala Leu Glu Glu Thr Phe Arg Ile Gly
231 225                               230                               235                               240
234 Arg Glu Leu Asp Val Pro Val Val Ile Ser His His Lys Val Met Gly
235                               245                               250                               255
238 Gln Pro Asn Phe Gly Arg Ser Arg Glu Thr Leu Pro Leu Ile Glu Ala
239                               260                               265                               270
242 Ala Met Ala Arg Gln Asp Val Ser Leu Asp Ala Tyr Pro Tyr Val Ala
243                               275                               280                               285
246 Gly Ser Thr Met Leu Lys Gln Asp Arg Val Leu Leu Ala Gly Arg Thr
247                               290                               295                               300
250 Ile Ile Thr Trp Cys Lys Pro Phe Pro Glu Leu Ser Gly Arg Asp Leu
251 305                               310                               315                               320
254 Asp Glu Val Ala Ala Glu Arg Gly Lys Ser Lys Tyr Asp Val Val Pro
255                               325                               330                               335
258 Glu Leu Gln Pro Ala Gly Ala Ile Tyr Phe Met Met Asp Glu Pro Asp
259                               340                               345                               350
262 Val Gln Arg Ile Leu Ala Phe Gly Pro Thr Met Ile Gly Ser Asp Gly
263                               355                               360                               365
266 Leu Pro His Asp Glu Arg Pro His Pro Arg Leu Trp Gly Thr Phe Pro
267                               370                               375                               380
270 Arg Val Leu Gly His Tyr Ala Arg Asp Leu Gly Leu Phe Pro Leu Glu
271 385                               390                               395                               400
274 Thr Ala Val Trp Lys Met Thr Gly Leu Thr Ala Ala Arg Phe Gly Leu
275                               405                               410                               415
278 Ala Gly Arg Gly Gln Leu Gln Ala Gly Tyr Phe Ala Asp Leu Val Val
279                               420                               425                               430
282 Phe Asp Pro Ala Thr Val Ala Asp Thr Ala Thr Phe Glu His Pro Thr
283                               435                               440                               445
286 Glu Arg Ala Ala Gly Ile His Ser Val Tyr Val Asn Gly Ala Pro Val
287                               450                               455                               460
290 Trp Gln Glu Gln Ala Phe Thr Gly Gln His Ala Gly Arg Val Leu Ala
291 465                               470                               475                               480
294 Arg Thr Ala Ala

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VERIFICATION SUMMARY

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Input Set : A:\217301US0PCT.txt

Output Set: N:\CRF3\01142002\J009782.raw

L:13 M:270 C: Current Application Number differs, Replaced Current Application No

L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date